

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/581,293
Source: IFWP
Date Processed by STIC: 7/17/06

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IFWP

RAW SEQUENCE LISTING

DATE: 07/17/2006

PATENT APPLICATION: US/10/581,293

TIME: 11:09:23

Input Set : F:\Final Sequence list-12810-00252-US.txt

Output Set: N:\CRF4\07172006\J581293.raw

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3 <110> APPLICANT: Ehrhardt, Thomas
4   Reindl, Andreas
5   Freund, Annette
6   Schmidt, Ralf-Michael
7   Sonnewald, Uwe
8   Sitt Nigel, Marc
9   Lein, Wolfgang
10  Bornke, Frederik
11  Deist, Kirsten
14 <120> TITLE OF INVENTION: Clp-protease as target for herbicides
17 <130> FILE REFERENCE: 12810-00252-US
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/581,293
C--> 19 <141> CURRENT FILING DATE: 2006-06-01
19 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/0013555
20 <151> PRIOR FILING DATE: 2004-11-30
22 <150> PRIOR APPLICATION NUMBER: EP 03027637.2
23 <151> PRIOR FILING DATE: 2003-12-02
25 <160> NUMBER OF SEQ ID NOS: 33
27 <170> SOFTWARE: PatentIn version 3.3
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 591
32 <212> TYPE: DNA
33 <213> ORGANISM: Arabidopsis thaliana
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)..(591)
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42 Met Pro Ile Gly Val Pro Lys Val Pro Phe Arg Ser Pro Gly Glu Gly
43 1          5          10          15
45 gat aca tct tgg gtt gac ata tac aac cga ctt tat cga gaa aga tta      96
46 Asp Thr Ser Trp Val Asp Ile Tyr Asn Arg Leu Tyr Arg Glu Arg Leu
47          20          25          30
49 ttt ttt tta ggc caa gag gtt gat acc gaa atc tcg aat caa ctt att      144
50 Phe Phe Leu Gly Gln Glu Val Asp Thr Glu Ile Ser Asn Gln Leu Ile
51          35          40          45
53 agt ctt atg ata tat ctc agt ata gaa aag gat acc aaa gat ctt tat      192
54 Ser Leu Met Ile Tyr Leu Ser Ile Glu Lys Asp Thr Lys Asp Leu Tyr
55          50          55          60
57 ttg ttt ata aac tct cct ggt gga tgg gta ata tct gga atg gct att      240
58 Leu Phe Ile Asn Ser Pro Gly Gly Trp Val Ile Ser Gly Met Ala Ile
59 65          70          75          80
61 tat gat act atg caa ttt gtg cga ccc gat gta cag aca ata tgc atg      288

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62 Tyr Asp Thr Met Gln Phe Val Arg Pro Asp Val Gln Thr Ile Cys Met
63      85      90      95
65 gga ttg gcc gct tca ata gca tcc ttt atc cta gtc gga gga gca att      336
66 Gly Leu Ala Ala Ser Ile Ala Ser Phe Ile Leu Val Gly Gly Ala Ile
67      100      105      110
69 acc aaa cgt ata gca ttc cct cac gct agg gta atg atc cat caa ccc      384
70 Thr Lys Arg Ile Ala Phe Pro His Ala Arg Val Met Ile His Gln Pro
71      115      120      125
73 gct agt tcg ttt tat gag gca caa acg gga gaa ttt atc ttg gaa gcg      432
74 Ala Ser Ser Phe Tyr Glu Ala Gln Thr Gly Glu Phe Ile Leu Glu Ala
75      130      135      140
77 gaa gaa tta ctt aaa ctt cgc gaa acc atc aca agg gtt tat gta caa      480
78 Glu Glu Leu Leu Lys Leu Arg Glu Thr Ile Thr Arg Val Tyr Val Gln
79 145      150      155      160
81 aga acg ggc aaa cct ata tgg gtt ata tcc gaa gac atg gaa cgg gat      528
82 Arg Thr Gly Lys Pro Ile Trp Val Ile Ser Glu Asp Met Glu Arg Asp
83      165      170      175
85 gtt ttt atg tca gca aca gaa gcc caa gct cat gga att gtt gat ctt      576
86 Val Phe Met Ser Ala Thr Glu Ala Gln Ala His Gly Ile Val Asp Leu
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89 gta gcg gtt caa taa      591
90 Val Ala Val Gln
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95 <211> LENGTH: 196
96 <212> TYPE: PRT
97 <213> ORGANISM: Arabidopsis thaliana
99 <400> SEQUENCE: 2
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102 1      5      10      15
105 Asp Thr Ser Trp Val Asp Ile Tyr Asn Arg Leu Tyr Arg Glu Arg Leu
106      20      25      30
109 Phe Phe Leu Gly Gln Glu Val Asp Thr Glu Ile Ser Asn Gln Leu Ile
110      35      40      45
113 Ser Leu Met Ile Tyr Leu Ser Ile Glu Lys Asp Thr Lys Asp Leu Tyr
114      50      55      60
117 Leu Phe Ile Asn Ser Pro Gly Gly Trp Val Ile Ser Gly Met Ala Ile
118 65      70      75      80
121 Tyr Asp Thr Met Gln Phe Val Arg Pro Asp Val Gln Thr Ile Cys Met
122      85      90      95
125 Gly Leu Ala Ala Ser Ile Ala Ser Phe Ile Leu Val Gly Gly Ala Ile
126      100      105      110
129 Thr Lys Arg Ile Ala Phe Pro His Ala Arg Val Met Ile His Gln Pro
130      115      120      125
133 Ala Ser Ser Phe Tyr Glu Ala Gln Thr Gly Glu Phe Ile Leu Glu Ala
134      130      135      140
137 Glu Glu Leu Leu Lys Leu Arg Glu Thr Ile Thr Arg Val Tyr Val Gln
138 145      150      155      160
141 Arg Thr Gly Lys Pro Ile Trp Val Ile Ser Glu Asp Met Glu Arg Asp

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149 Val Ala Val Gln
150          195
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154 <211> LENGTH: 1024
155 <212> TYPE: DNA
156 <213> ORGANISM: Nicotiana tabacum
158 <220> FEATURE:
159 <221> NAME/KEY: CDS
160 <222> LOCATION: (11)..(877)
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165          Met Ala Val Thr Phe Pro Thr Thr Ser Ser Ser Tyr Leu
166          1          5          10
168 cac tcg aga act aaa gtc cct cag cct tct tta agc tgc gcc agc aaa      97
169 His Ser Arg Thr Lys Val Pro Gln Pro Ser Leu Ser Cys Ala Ser Lys
170          15          20          25
172 gtt ttt gtc gga tta aga agc caa tct cct aat tct tat ggg att gca      145
173 Val Phe Val Gly Leu Arg Ser Gln Ser Pro Asn Ser Tyr Gly Ile Ala
174 30          35          40          45
176 gcg tct aat gta aat gtt gaa ttt cac aat aga gtg tac aga agt att      193
177 Ala Ser Asn Val Asn Val Glu Phe His Asn Arg Val Tyr Arg Ser Ile
178          50          55          60
180 gaa tcc gga act aga gac agt aaa cca aca cgt gta cga gtt tcc atg      241
181 Glu Ser Gly Thr Arg Asp Ser Lys Pro Thr Arg Val Arg Val Ser Met
182          65          70          75
184 atg ccc att ggg aca cca aga gta ccc tac aga aat cca act gag gga      289
185 Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Pro Thr Glu Gly
186          80          85          90
188 aca tgg cag tgg gtt gat ttg tgg aat gct ctt tac cgt gaa cgt gtt      337
189 Thr Trp Gln Trp Val Asp Leu Trp Asn Ala Leu Tyr Arg Glu Arg Val
190          95          100          105
192 att ttc atc gga caa cac ata gat gaa gaa ttt agc aac cag ata ttg      385
193 Ile Phe Ile Gly Gln His Ile Asp Glu Glu Phe Ser Asn Gln Ile Leu
194 110          115          120          125
196 gca aca atg ctg tat ctt gac agt att gat gat tcc aag aag ctc tac      433
197 Ala Thr Met Leu Tyr Leu Asp Ser Ile Asp Asp Ser Lys Lys Leu Tyr
198          130          135          140
200 ctg tat atc aat ggc cct ggt ggt gat cta act cca agc atg gcc atc      481
201 Leu Tyr Ile Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser Met Ala Ile
202          145          150          155
204 tac gac aca atg caa agt ctt aaa agt gct gtt ggc acc cat tgt gtg      529
205 Tyr Asp Thr Met Gln Ser Leu Lys Ser Ala Val Gly Thr His Cys Val
206          160          165          170
208 ggc tat gcc tac aat ctt gcc ggt ttt ctt ctt gct gct gga gaa aag      577
209 Gly Tyr Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala Gly Glu Lys
210          175          180          185

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212 ggc aat cga ttt gca atg cct ctt tca agg att gca cta caa tct cca      625
213 Gly Asn Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu Gln Ser Pro
214 190                      195                      200                      205
216 gct gga gct gcg cgc gga cag gct gat gat att cgc aat gaa gca gat      673
217 Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Arg Asn Glu Ala Asp
218                      210                      215                      220
220 gaa ctt ctc aga att aga gat tac ctt ttc aag gag ttg gct gag aag      721
221 Glu Leu Leu Arg Ile Arg Asp Tyr Leu Phe Lys Glu Leu Ala Glu Lys
222                      225                      230                      235
224 aca ggc cag cct gtt gaa aag gtt cac aag gat tta agt cgg atg aag      769
225 Thr Gly Gln Pro Val Glu Lys Val His Lys Asp Leu Ser Arg Met Lys
226                      240                      245                      250
228 cga ctc aat gct caa gaa gct ctt gaa tat ggt ctt ata gac cgt ata      817
229 Arg Leu Asn Ala Gln Glu Ala Leu Glu Tyr Gly Leu Ile Asp Arg Ile
230                      255                      260                      265
232 gtt agg cct ccc cgt att aag gca gat gct cca cga aag gat acc aca      865
233 Val Arg Pro Pro Arg Ile Lys Ala Asp Ala Pro Arg Lys Asp Thr Thr
234 270                      275                      280                      285
236 gca ggt ctt ggt tagtccatac acatcgtata atttatggct gatagtgggt      917
237 Ala Gly Leu Gly
240 gtacgacttg cagtgttatt ttgcaatttc ttttgtttaa tctacatatt gaactctttt      977
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246 <211> LENGTH: 289
247 <212> TYPE: PRT
248 <213> ORGANISM: Nicotiana tabacum
250 <400> SEQUENCE: 4
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256 Thr Lys Val Pro Gln Pro Ser Leu Ser Cys Ala Ser Lys Val Phe Val
257                      20                      25                      30
260 Gly Leu Arg Ser Gln Ser Pro Asn Ser Tyr Gly Ile Ala Ala Ser Asn
261                      35                      40                      45
264 Val Asn Val Glu Phe His Asn Arg Val Tyr Arg Ser Ile Glu Ser Gly
265                      50                      55                      60
268 Thr Arg Asp Ser Lys Pro Thr Arg Val Arg Val Ser Met Met Pro Ile
269 65                      70                      75                      80
272 Gly Thr Pro Arg Val Pro Tyr Arg Asn Pro Thr Glu Gly Thr Trp Gln
273                      85                      90                      95
276 Trp Val Asp Leu Trp Asn Ala Leu Tyr Arg Glu Arg Val Ile Phe Ile
277                      100                     105                     110
280 Gly Gln His Ile Asp Glu Glu Phe Ser Asn Gln Ile Leu Ala Thr Met
281                      115                     120                     125
284 Leu Tyr Leu Asp Ser Ile Asp Asp Ser Lys Lys Leu Tyr Leu Tyr Ile
285                      130                     135                     140
288 Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser Met Ala Ile Tyr Asp Thr
289 145                     150                     155                     160
292 Met Gln Ser Leu Lys Ser Ala Val Gly Thr His Cys Val Gly Tyr Ala
293                      165                     170                     175

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296 Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala Gly Glu Lys Gly Asn Arg
297          180          185          190
300 Phe Ala Met Pro Leu Ser Arg Ile Ala Leu Gln Ser Pro Ala Gly Ala
301          195          200          205
304 Ala Arg Gly Gln Ala Asp Asp Ile Arg Asn Glu Ala Asp Glu Leu Leu
305          210          215          220
308 Arg Ile Arg Asp Tyr Leu Phe Lys Glu Leu Ala Glu Lys Thr Gly Gln
309 225          230          235          240
312 Pro Val Glu Lys Val His Lys Asp Leu Ser Arg Met Lys Arg Leu Asn
313          245          250          255
316 Ala Gln Glu Ala Leu Glu Tyr Gly Leu Ile Asp Arg Ile Val Arg Pro
317          260          265          270
320 Pro Arg Ile Lys Ala Asp Ala Pro Arg Lys Asp Thr Thr Ala Gly Leu
321          275          280          285
324 Gly
328 <210> SEQ ID NO: 5
329 <211> LENGTH: 1124
330 <212> TYPE: DNA
331 <213> ORGANISM: Arabidopsis thaliana
333 <220> FEATURE:
334 <221> NAME/KEY: CDS
335 <222> LOCATION: (2)..(931)
337 <400> SEQUENCE: 5
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341 1          5          10          15
343 tgt cta cta aac cct gga aaa aac ctt aat ttc cca atc cga aac cat      97
344 Cys Leu Leu Asn Pro Gly Lys Asn Leu Asn Phe Pro Ile Arg Asn His
345          20          25          30
347 aga atc cct aaa act tcg aaa ccc ttt tgc gtt agg tct tca atg agc      145
348 Arg Ile Pro Lys Thr Ser Lys Pro Phe Cys Val Arg Ser Ser Met Ser
349          35          40          45
351 ttg tct aaa cca ccc aga caa acc tta tct agt aac tgg gat gta tct      193
352 Leu Ser Lys Pro Pro Arg Gln Thr Leu Ser Ser Asn Trp Asp Val Ser
353          50          55          60
355 agc ttc tcc att gat tcc gtt gct caa tct cct tca aga ctc cca agt      241
356 Ser Phe Ser Ile Asp Ser Val Ala Gln Ser Pro Ser Arg Leu Pro Ser
357 65          70          75          80
359 ttc gaa gaa ctc gat acc acc aac atg ttg ctc cgt caa aga atc gtc      289
360 Phe Glu Glu Leu Asp Thr Thr Asn Met Leu Leu Arg Gln Arg Ile Val
361          85          90          95
363 ttt ttg ggt tct cag gtt gat gat atg acg gcg gat ttg gtt ata agt      337
364 Phe Leu Gly Ser Gln Val Asp Asp Met Thr Ala Asp Leu Val Ile Ser
365          100          105          110
367 cag cta ttg tta cta gat gct gag gac tca gaa aga gac att acg ctt      385
368 Gln Leu Leu Leu Leu Asp Ala Glu Asp Ser Glu Arg Asp Ile Thr Leu
369          115          120          125
371 ttt atc aat tca ccc ggt gga tct att act gct ggg atg gga ata tat      433
372 Phe Ile Asn Ser Pro Gly Gly Ser Ile Thr Ala Gly Met Gly Ile Tyr

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VERIFICATION SUMMARY

DATE: 07/17/2006

PATENT APPLICATION: US/10/581,293

TIME: 11:09:24

Input Set : F:\Final Sequence list-12810-00252-US.txt

Output Set: N:\CRF4\07172006\J581293.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application No

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date